REMARKS

Entry of the foregoing, examination and favorable consideration of the subject application in light of the following remarks are respectfully requested.

By the foregoing amendment, the specification has been amended to insert the appropriate sequence identifiers. Further, the specification has been amended to insert the attached copy of the sequence listing after the last page of the disclosure (currently page 36) and before the claims (currently page 46). Please renumber the pages accordingly. Claims 2-24 have been canceled without prejudice or disclaimer of the subject matter recited therein. Further, claim 1 has been amended to further clarify Applicant's invention. Support for the amendments can be found throughout the specification. Accordingly, no new matter has been added.

In view of the foregoing, further and favorable action in the form of a Notice of Allowance is believed to be next in order. Such action is earnestly solicited.

In the event that there are any questions relating to this application, it would be appreciated if the Examiner would telephone the undersigned attorney concerning such questions so that prosecution of this application may be expedited.

Respectfully submitted,

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Date: December 21, 2001

Attachment to Amendment dated December 21, 2001
Marked-up Claim

1. (Amended) An isolated DNA sequence [capable of] serving as a genetic regulatory element in a chimeric gene, wherein said DNA sequence is the first intron (intron 1) of the 5' non-translated region of a plant H3.3 histone gene [which can be used for the transformation of plants and allowing the expression of the product of translation of the chimeric gene in particular in the regions of the plant undergoing rapid growth, characterized in that it comprises at least one intron such as the first intron (intron 1) of the noncoding 5' region of a plant histone gene].

Attachment to Amendment dated December 21, 2001

Marked-up Specification

Paragraph beginning at page 11, line 8:

EXAMPLE 1:

1. Production of an EPSPS fragment from Arabidopsis thaliana

a) two 20-mer oligonucleotides of respective sequences (SEQ ID NOS:8 and 9):

5'-GCTCTGCTCATGTCTGCTCC-3'

5'-GCCCGCCCTTGACAAAGAAA-3'

were synthesized from the sequence of an EPSPS gene from Arabidopsis thaliana (Klee H.J. et al., (1987) Mol. Gen. Genet., 210, 437-442). These two oligonucleotides correspond to positions 1523 to 1543 and 1737 to 1717, respectively, of the published sequence and in convergent orientation.

Paragraph beginning at page 13, line 3:

Two single-stranded and partially complementary oligonucleotides of respective sequences (SEQ ID NO:10):

5'-AATTCCCGGG-3'

5'-CCCGGG-3' (the latter being phosphorylated)

are ligated to double-stranded cDNAs with blunt ends.

Paragraph beginning at page 20, line 11:

The plasmid DNA content of the various clones was analysed according to the procedure described for pRPA-ML-711. One of the plasmid clones retained contains an EcoRI-HindIII insert of about 1.45 kbp. The sequence of the terminal ends of this clone shows that the 5' end of the insert corresponds exactly to the corresponding end of pRPA-ML-711 and that the 3' terminal end has the following sequence (SEQ ID NO:11):

"5'...AATAAGCTCTAGAGTCGACCTGCAGGCATGCAAGCTT-3'".

Paragraph beginning at page 21, line 3:

The clone pRPA-ML-712 was cut with the restriction enzymes PstI and HindIII. The DNA resulting from these manipulations was separated by electrophoresis on a 0.8 % LGTA/TBE agarose gel (ref. CPMB). The gel fragment containing the PstI/EcoRI insert of 1.3 kbp was excised from the gel and purified according to the procedure described in paragraph 5 above. This insert was ligated in the presence of an equimolar quantity of each of the two partially complementary oligonucleotides of sequence (SEQ ID NOS:12 and 13):

Oligo 1: 5'-GAGCCGAGCTCCATGGCCGGCGCCGAGGAGATCGTGCTGCA-3'

Oligo 2: 5'-GCACGATCTCCTCGGCGCCGGCCATGGAGCTCGGCTC-3'

as well as in the presence of DNA from the plasmid pUC19 digested with the restriction enzymes BamHI and HindIII.

Paragraph beginning at page 24, line 16:

The sequence of pRPA-ML-715 is arbitrarily numbered by placing the first base of the N-terminal alanine codon GCC in position 1. This sequence has an NcoI site in position 1217. The site-modifying oligonucleotide has the sequence (SEQ ID NO:14):

5'-CCACAGGATGGCGATGGCCTTCTCC-3'.

Paragraph beginning at page 25, line 7:

The following oligonucleotides (SEQ ID NOS:15, 16, 17 and 18) were used:

a) Thr 102 → Ile mutation.

5'-GAATGCTGGAATCGCAATGCGGCCATTGACAGC-3'

b) Pro 106 → Ser mutation.

5'-GAATGCTGGAACTGCAATGCGGTCCTTGACAGC-3'

c) Gly 101 → Ala and Thr 102 → Ile mutations.

5'-CTTGGGGAATGCTGCCATCGCAATGCGGCCATTG-3'

d) Thr 102 → Ile and Pro 106 → Ser mutations.

5'GGGGAATGCTGGAATCGCAATGCGGTCCTTGACAGC-3'

Paragraph beginning at page 26, line 17:

A DNA fragment of 418 base pairs is purified from digestion of the cosmid clone c22 with the restriction enzyme DdeI followed by treatment with a Klenow fragment of DNA polymerase from E. coli, according to the manufacturer's instructions for creating a blunt-ended

DNA fragment and then cut with MseI. The purified DNA fragment is ligated to a synthetic oligonucleotide adaptor having the following sequence (SEQ ID NOS:19 and 20):

Adaptor 1: 5' TAATTTGTTGAACAGATCCC 3'

TAAACAACTTGTCTAGGG

Paragraph beginning at page 27, line 5:

3. Intron No. 2:

A DNA fragment of 494 base pairs is purified from the digestion of the cosmid clone c22 with the restriction enzymes AluI and CfoI. The purified DNA fragment is ligated to a synthetic oligonucleotide adaptor having the following sequence (SEQ ID NOS:21 and 22):

Adaptor 2: 5' CAGATCCCGGGATCTGCG 3'

GCGTCTAGGGCCCTAGACGC